

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1035.2	51.3	3117	4	US-09-146-580-6		Sequence 6, Appli
2	475.6	23.6	484	4	US-09-621-976-1513		Sequence 153, Appli
3	379	18.8	381	4	US-09-146-580-7		Sequence 7, Appli
C 4	302	15.0	311	4	US-09-146-580-11		Sequence 11, Appli
C 5	230	11.4	35060	3	US-09-814-095-2		Sequence 7, Appli
6	224	11.1	42571	4	US-09-810-347-3		Sequence 3, Appli
C 7	223.6	11.1	392000	4	US-10-027-983-11		Sequence 11, Appli
C 8	220.4	10.9	18853	4	US-09-820-005-3		Sequence 3, Appli
C 9	220.2	10.9	685	4	US-09-183-266A-16		Sequence 16, Appli
C 10	220.2	10.9	1332	4	US-09-584-568C-1		Sequence 1, Appli
C 11	219.2	10.9	5298	4	US-09-491-356C-1		Sequence 1, Appli
C 12	224	10.8	4108	4	US-09-883-096-1		Sequence 1, Appli
C 13	218.6	10.8	2839	3	US-09-701-702-10		Sequence 1, Appli
C 14	217.4	10.8	98844	3	US-09-679-409-1		Sequence 10, Appli
C 15	217	10.8	8453	3	US-09-167-681-45		Sequence 45, Appli
C 16	216.8	10.7	118067	4	US-09-497-855A-32		Sequence 32, Appli
C 17	216.4	10.7	631	3	US-09-385-982-354		Sequence 1, Appli
C 18	216.4	10.7	1426	4	US-09-620-312D-967		Sequence 967, Appli
C 19	216.4	10.7	319608	4	US-09-539-333D-1		Sequence 1, Appli
C 20	216.4	10.7	319608	4	US-09-679-409-1		Sequence 1, Appli
C 21	214.8	10.6	74962	4	US-09-685-853A-3		Sequence 3, Appli
C 22	214.6	10.6	21784	4	US-09-820-002-3		Sequence 3, Appli
C 23	214.4	10.6	6231	3	US-09-623-655-1203		Sequence 1203, Appli
C 24	214.4	10.6	21968	4	US-09-851-985-3		Sequence 3, Appli
C 25	214.4	10.6	63000	4	US-09-780-172-18		Sequence 18, Appli
C 26	213.6	10.6	128779	4	US-09-497-855A-38		Sequence 38, Appli
C 27	213.2	10.6	1701	3	US-09-078-294-9		Sequence 9, Appli

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Db	1969	CTGATATGAAAGAACAAAAGCCCTGCTTCTGCCAGAACCTTGCCTCCCACT 2028		Sequence 1513, Application US/09621976
Qy	1031	CAGTTCTTGGAGCAGCTTAAGGGCCCAAGATGGCTCGCTCTGGATGTTTA 1090		Patent No. 66,903
Db	2029	NAGTTCTTGGNCAGNACTAGTGGCCTTGGCTTNGKGTGTGATTAA 2088		GENERAL INFORMATION:
Qy	1091	CGCTCTCCTAAACAGAGCTACATCTTACGCTTACACCTCTCACAGTT 1150		APPLICANT: Dumas Milne Edwards, J. B.
Db	2089	NGYTCTGCTTAAACAGNGCNWACATTTAGCTCTACCTCCACCTTCTNAMGTT 2148		APPLICANT: Giordano, J. Y.
Qy	1151	TTTGTGTTGGTTGGTTTTTGAGACAGAGCTCACTCTG-TTGCCTGGCTGG 1209		TITLE OF INVENTION: ESTs and Encoded Human Proteins.
Db	2149	TTTGTGTTKGTTGTTGTTGAGACAGRTNTNAYCTGTTGCCARGTGG 2207		FILE REFERENCE: GENSET_054 PR2
Qy	1210	AG-TGCACTGGCAACAATCTCGGCT-CATTGCAACCTCCGCC-CGTTCAAGGGAT 1265		CURRENT FILING DATE: 2000-07-21
Db	2208	ARTTGCGTGGACAAYTNGGTCACYTNGCTCCSSCGTCAKGAT 2267		NUMBER OF SEQ ID NOS: 19335
Qy	1266	TCTCTTGCTCTGACCTT-CCCAAGTAACTGATATTACGGGCCACACCCGC 1324		SEQ ID NO: 1513
Db	2268	YTCCTTGCTCYTCACGCTCCCAAGTAANTGATATTACGGGCCACACCCGN 2327		LENGTH: 84
Qy	1325	TGATTTTGTTATTGTTAGAGACGGGGTTTCCAGTGTGGCTGGCTAAC 1384		TYPE: DNA
Db	2328	TGAWTTTGTTGTTTARTARAMGGGTTTCCCGCCTGNGGCTGTCTNAAAN 2387		ORGANISM: Homo sapiens
Qy	1385	T-CTTGACTCAAGTGAACCAACCCGCTGTGCTCCAAAGTGTGAAATTACCGGG-T 1442		FEATURE: CDS
Db	2388	TCTTGACNTCAKTAACGACCCGCTGTGCTTCAAATGCTGAAATTACCGGT 2447		LOCATION: 77..457
Qy	1443	GGCCCAATATGGGGCTCACAGTTGCTTGTGACATTCTCTTGTGG 1501		NAME/KEY: sig_peptide
Db	2448	GAACCAACATGGGGCYCACAGTTGTCATTTGAACTTGTGAAATTGGTGG 2507		LOCATION: 77..133
Qy	1552	CCTCTTTTGTGCTCATAGGGCTCAAGATAGTAAAGGCCCTGAGT-GTTGATA 1560		OTHER INFORMATION: Von Heine matrix
Db	2508	CTTYYTTTNNCCATAGNNGCTTCAAGATAGTAAAGRGCCCTGAGTGTCTWTA 2567		OTHER INFORMATION: score 6..80000019073486
Qy	1561	AGAGCCAAATAGAGCAAGGGCCACHTTA--TCAGTTGGCAAGTGTCCGGCCTCC 1618		OTHER INFORMATION: seq AIVALAVRALHA/SE
Db	2568	RGAAGCMMATAGRANERGGARCANNTTNTACGGTGGCAAGTGTCCNNNGCYTCT 2627		US-09-621-976-1513
Qy	1619	GCTGGCTAGTCCAAGGCGTGGCTGGAGGATGTCTGGACATGGACACAC 1678		Query Match 23..68; Score 475..6; DB 4;
Db	2628	GCTGTTTNTCCAGGCGTGGTGGCAARGANKNTTGGARTGTAAATGGANANAC 2687		Best Local Similarity 99.8%; Pred. No. 2..8e-100;
Qy	1679	-AGAGGCAACTGAGTGTCTCATAGGTAAATGCCACAAAAGTGGCTT-GCCTAAAT 1735		Matches 475; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db	2688	CAGNAGGNCCTGAGTGCYNNNTAGGTAAATGCAAAACTGGCTTGGCTATAT 2747		Qy 70 AAGGACACCTTGTGCCTCATTCCTGTGATGAAACAGCTTCACTTGTGTCAGTGC 1.29
Qy	1736	CCCTCATGCACTTGTGATTGCAATTAAATTATTTCTGACATTGTGCAAG-CTTGTG 1794		Db 1 AAGGACACCTTGTGCCTCATTCCTGTGATGAAACAGCTTCACTTGTGTCAGTGC 6.0
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Qy	1795	TATTATATTTCACCTTATAGTGGAGAAATTGGCTCTTAGGGTAAATGTGCTTG 1854		Db 61 ATGAGGGCAGGAGGAAATGCAAGGAGGACTGCCTATGCTGTCAGTGC 1.20
Db	2808	TTTTTTTATTTCNNCTNTACGGGCTGGTGGTGGCAAGTGTAAATGANTTG 2867		Qy 190 GGCCCTCATGGCTCAAGGCCAACTTCCATGCTCCAGCTGCTTCCAGCTGCTGTCAGTGC 2.49
Qy	1855	CCCAGGT-CACATAGGAGTGGCAAGAACAGCTTAAATGAAATTAAATAAAA 1913		Db 121 GGCCTCTCATGGCTCAAGGCCAACTTCCATGCTCCAGCTGCTTCCAGCTGTCAGTGC 1.80
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Qy	1914	TATATATGAGTAACTTAAATATAACCAATTTAAATTAACTTAAACGTC 1973		Db 181 ACATCATATTCCAGAGGGCTCTGGAAAGAGTGTGATTCAGAGTGAATAATGCTGCACTTGTGTCAGTGC 2.40
Qy	2928	TATATATGAGTAACTTAAATATAACCAATTTAAATTAACTTAAACGTC 2987		Qy 310 TGGGGATGTGACTTGGCTGCTCATCTTGTGCTGTCATCTTGTGTCAGTGC 3.69
Db	2886	CNCNRGTTNACMAGGAACTGGCNRARAANCTTANATNGAAAAAATTAATAAA 2008		Db 241 TGGGGATGTGACTTGGCTGCTGTCATCTTGTGTCAGTGC 3.00
Qy	1974	TAACCAACATTAATAAAACTTGTACGAACTTAAACGTC 2008		Qy 370 CGCGCAZACCATACTGTAAAGCTGGATGAAAGTGCAGCTGCCAGAAAATGCTAA 4.29
Qy				Db 301 CGCGCAZACCATACTGTAAAGCTGGATGAAAGTGCAGCTGCCAGAAAATGCTAA 3.60
Qy				Qy 430 AGGAAATGTTGGCACAGGAAGAACCATGGCAAGGAGCAAGTACAGGCCACATCA 4.89
Qy				Db 361 AGGAAATGTTGGCACAGGAAGAACCATGGCAAGGAGCAAGTACAGGCCACATCA 4.20
Qy				RESULT 3
Qy				US-09-146-580-7
Qy				Sequence 7, Application US/09146580A
Qy				Patent No. 6306653
Qy				GENERAL INFORMATION:

APPLICANT: Papsidero, Lawrence D
 APPLICANT: Dyster, Lyn M
 TITLE OF INVENTION: DETECTION AND TREATMENT OF BREAST DISEASE
 CURRENT APPLICATION NUMBER: US/09/146, 580A
 CURRENT FILING DATE: 1998-09-03
 EARLIER APPLICATION NUMBER: 60/071, 889
 EARLIER FILING DATE: 1998-01-20
 EARLIER APPLICATION NUMBER: 60/092, 155
 EARLIER FILING DATE: 1998-07-09
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 7
 LENGTH: 381
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (207)
 OTHER INFORMATION: N at position 207 is either A, C, G, or T
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (272)
 OTHER INFORMATION: N at position 272 is either A, C, G, or T
 US-09-146-580-7

Query Match 18.8%; Score 379; DB 4; Length 381;
 Best Local Similarity 99.5%; Pred. No. 4.2e-78;
 Matches 379; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 147 TGCAGCAGAGGAGCTGGCATCGTGGCTCCAGGCTACATCCCTCG 205
 Db 1 TGGAGCAGGAGGACTGGCATCGTGGCTTGGCTACATGCCAG 60
 QY 207 AAGCCATACTCCATTGGCTCCAGCTGGCATCGGAGTTTCACATCATATTCCAGA 266
 Db 61 AAGCCATATCCCTCATGGCTCCATTGGCTCCAGCTGGCATCATATTCCAGA 120
 QY 267 GGCTCCCTGGAAAGGTGATAATGGTGGATCGATCCGGAGACTGATGGGTTGGGACTTGG 326
 Db 121 GGCTCCCTGGAAAGGTGATAATGGTGGATCGATCCGGAGCTGGGTTGGGACTTGG 180
 QY 327 CTGTGTCTCCCTCATGTCAGGCCGCAACACATCTGTCAGGCCGCAACACATCTG 386
 Db 181 CTGTGTCTCCCTCATGTCAGGCCGCAACACATCTGTCAGGCCGCAACACATCTG 240
 QY 387 TTAAGCAGTGGATGAAAGTGTCAAGCTGCCAGAAGAAATGGTAAGGAAATGGTTGCCACA 446
 Db 241 TTAAGCAGTGGATGAAAGTGTCAAGCTGCCAGAAGAAATGGTAAGGAAATGGTTGCCACA 300
 QY 447 GGAGAAACACCATGGCAAGAGGAACATACAGGGCAACATCAGGGAAACAGAAACAT 506
 Db 301 GGAGAAACACCATGGCAAGAGGAACATACAGGGCAACATCAGGGAAACAGAAACAT 360
 QY 507 ACGGCCATAAACACTCTTATT 527
 Db 361 ACGGCCATAAACACTCTTATT 381

RESULT 5
 US-09-146-580-11/C
 Sequence 11, Application US/09146580A
 Patent No. 6306653
 GENERAL INFORMATION:
 APPLICANT: Papsidero, Lawrence D
 APPLICANT: Dyster, Lyn M
 TITLE OF INVENTION: DETECTION AND TREATMENT OF BREAST DISEASE
 FILE REFERENCE: 200755/1/002
 CURRENT APPLICATION NUMBER: US/09/146, 580A
 CURRENT FILING DATE: 1998-09-03
 EARLIER APPLICATION NUMBER: 60/071, 889

RESULT 4
 US-09-146-580-11/C
 Sequence 11, Application US/09146580A
 Patent No. 6306653
 GENERAL INFORMATION:
 APPLICANT: Papsidero, Lawrence D
 APPLICANT: Dyster, Lyn M
 TITLE OF INVENTION: DETECTION AND TREATMENT OF BREAST DISEASE
 FILE REFERENCE: 200755/1/002
 CURRENT APPLICATION NUMBER: US/09/146, 580A
 CURRENT FILING DATE: 1998-09-03
 EARLIER APPLICATION NUMBER: 60/071, 889

Query Match 15.0%; Score 302; DB 4; Length 311;
 Best Local Similarity 99.3%; Pred. No. 2e-60;
 Matches 302; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 US-09-146-580-11

QY 208 AGCCATACTCCATTGCTCCAGGCTTCACATCATATTCCAGAG 267
 Db 311 AGCCATACTCCATTGCTCCAGGCTTCACATCATATTCCAGAG 252

Query Match 15.0%; Score 302; DB 4; Length 311;
 Best Local Similarity 99.3%; Pred. No. 2e-60;
 Matches 302; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 US-09-146-580-11

QY 268 GCTCTGGAAAGACTGAATATGGTGTGATGGATTGTGACTTGGC 327
 Db 191 TGCTGTCTCCATTGTAAGGAGAGAAATCTGTTCAAGGGCAACCATACTGT 132
 QY 328 TGCTGTCTCCATTGCTCCAGGCTTCACATCATATTCCAGAG 387
 Db 191 TGCTGTCTCCATTGTAAGGAGAGAAATCTGTTCAAGGGCAACCATACTGT 192
 QY 388 TAACAGTGGATGAAAGTGCAACTGCAAGAAATGTAANGAATGTTGCAAG 447
 Db 131 TAACAGTGGATGAAAGTGCAACTGCAAGAAATGTAANGAATGTTGCAAG 72
 QY 448 GAAGAAACACCATGGCAAGAGGAACAGTAAACAGGCACATCAGGGAAACACGAAACATA 507
 Db 71 GAAGAAACACCATGGCAAGAGGAACATGAACTACAGGGCAATCAGGGAAACACGAAACATA 12
 QY 508 CGGC 511
 Db 11 CGGC 8

RESULT 5
 US-09-146-095-7/C
 Sequence 7, Application US/08814095
 Patent No. 6025183
 GENERAL INFORMATION:
 APPLICANT: Soreq, Hermona
 APPLICANT: Zakut, Haim
 APPLICANT: Shani, Moshe
 TITLE OF INVENTION: TRANSSENIC ANIMAL ASSAY SYSTEM FOR
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: KOEN & ASSOCIATES
 STREET: 30500 No. 6025183thwestern Highway, Suite 410
 CITY: Farmington Hills
 STATE: Michigan
 COUNTRY: U.S.
 ZIP: 48334
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/B14, 095

FILING DATE: 800
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Montgomery, Ilene N.
 REGISTRATION NUMBER: 38.972
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (248) 539-5050
 TELEFAX: (248) 539-5055
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 35060 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "Cosmid including ACHE
 HYPOTHETICAL: promoter, ACHE gene and ARS gene"
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 POSITION IN GENOME:
 CHROMOSOME/SEGMENT: 7q22
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 NAME/KEY: promoter
 LOCATION: 4085..22464
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 OTHER INFORMATION: /standard_name= "ACHE Promotor"
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 NAME/KEY: exon
 LOCATION: 22465..22537
 OTHER INFORMATION: /function= "non-translated"
 OTHER INFORMATION: /gene= "ACHE"
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 NAME/KEY: exon
 LOCATION: 24090..25177
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 OTHER INFORMATION: /function= "translation start"
 OTHER INFORMATION: 24110"
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 NAME/KEY: exon
 LOCATION: 25524..26009
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 OTHER INFORMATION: /evidence= EXPERIMENTAL
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 NAME/KEY: exon
 LOCATION: 27005..27274
 IDENTIFICATION METHOD: experimental
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 OTHER INFORMATION: /gene= "ACHE"
 OTHER INFORMATION: /number= 4
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 NAME/KEY: terminator
 LOCATION: 27385..27387
 NAME/KEY: exon
 LOCATION: 28008..28129
 IDENTIFICATION METHOD: experimental
 OTHER INFORMATION: /evidence= EXPERIMENTAL

; PRIOR APPLICATION NUMBER: PCT/US99/09365
 ; PRIOR FILING DATE: 1999-04-29
 ; PRIOR APPLICATION NUMBER: 60/083,465
 ; PRIOR FILING DATE: 1998-04-29
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 1
 ; LENGTH: 55298
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 ; ORGANISM: Homo sapiens
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 ; NAME/KEY: misc feature
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 ; OTHER INFORMATION: n is not determined
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Query Match 10.9%; Score 219.2; DB 4; Length 55298;
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 Db 42815 TTCTGAGCAGTGAACCATTAGGGTTCACTCTAAGTGTCTTCTTCTTCTT 42874

Qy 1156 TGTGTTGGTTGGTTGGTTGGAGAGAGCTACTCTTGCCAGGGTGGACTGCA 1215
 Db 42875 CTTTTTCTTCTTCTTCTTCTTGTAGAGAGTCTCCTCTGCTGAGGTGGTGTGCA 42934

Qy 1216 GTGGCAAAATCTGGCTCATGCAACTCCGGCTCCGGCTCAAGTGTCTCTGCC 1275
 Db 42935 ATGGATGATCTGGCTACTACAACCTCCGGTTAAAGCAATCTCCGGCT 42994

Qy 1276 CAGCTCTCAAGTAATCTGATATTACGGGCGCAGGACACACCCGGCTATTTGTA 1335
 Db 42995 CAGCCTCCAGTAGTGGGTTACGGGTTACGGGCTTACGGGCACTACGGCTATTTGTA 43053

Qy 1336 TTTTTAGAGAGCAGGGTTTCCAGTGGCTCAAACTTGTGACTCTGACTCA 1395
 Db 43054 TTTTTAGAGAGCAGGGTTACCATGTTGGCAAGTGTGGCTCTGACTCTGACTCA 43113

Qy 1396 AGTGAACACGGCCCTGCTGCCAAAGTGTGGAAATTACAGGCTGAGCCACATGCC 1455
 Db 43114 GTGTGATCACCTGGCTTGGCTGGGTTAAAGGTGTGCCATGTTCTTCTTCTT 3353

Qy 1456 GGGC 1459

Db 43174 CAGC 43177

RESULT 12
 ; Sequence 1, Application US/09883096
 ; Patent No. 6680369
 ; GENERAL INFORMATION:
 ; APPLICANT: Beraud, Christophe
 ; APPLICANT: Craven, Andrew
 ; APPLICANT: Yu, Ming
 ; APPLICANT: Sakowicz, Roman
 ; APPLICANT: Patel, Umesh A.
 ; APPLICANT: Davies, Katherine A.
 ; TITLE OF INVENTION: NOVEL MOTOR PROTEINS AND METHODS FOR THEIR USE
 ; FILE REFERENCE: 010552-01410US
 ; CURRENT APPLICATION NUMBER: US/09/883,096
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: US 09/594,655
 ; PRIOR FILING DATE: 2000-06-15
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 1
 ; LENGTH: 4108
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Nucleic acid sequence of human kinesin motor
 ; OTHER INFORMATION: protein gene Hskip3a (Figure 1).
 ; OTHER INFORMATION: Description of Artificial Sequence: Hskip3a gene.
 ; US-09-883-096-1

Query Match 10.8%; Score 218.6; DB 4; Length 4108;
 Best Local Similarity 76.7%; Pred. No. 6.8e-41; Indels 1; Gaps 1;
 Matches 280; Conservative 0; Mismatches 84; Indels 1;

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 Db 2995 GTGGTTTGTGTTGGTTGGTTGGTTGGATGGATGGTCTACTCTGTTGCCCCAGGCT 3054

Qy 1208 GGAGTCAGTGGCACATCTGGCTCATGGACCTCCGGCTTCCGGCTTCAAGTGATTC 1267
 Db 3055 GGAGTCAGTGGTACATCTGGCTCATGGTCTACTGAACTCCGGCTTCAAGTGATTC 3114

Qy 1268 TCTGCTCAGCCCTCCAGTAATCTGATGGTGGATTACAGGCCCCCTGA 1327
 Db 3115 TCTGCTCAGCTTCAAGTGGTGGATTACAGGCCCCCTGA 3173

Qy 1328 TTTTGTTATTTTGTAGAGAGCAGGGTTTCCACGTTGGCTTCAAACTCT 1387
 Db 3174 TTTCTCTCTTAAATAGAGGGGGTTTCCATTTGGCAGGGTCTTGAACTCC 3233

Qy 1388 TGACCTCAAGTGAACACCCGGCTGCTCCAAAGTGTGGAAATTACAGGCTGAGCC 1447
 Db 3234 TGACCTCAAGTGGTGTCTGGCTCTCCCTGCTTCAAGTGGATTAACGGCTAGCT 3293

Qy 1448 ACCATTCGGGCTCAAGCTTGTGATACCTCTCTCTCTCTCTCTCTCTCTCT 1507
 Db 3294 ACCACGCTGGCCCTGGTGTGTTAAAGGTGTGCCATGTTCTTCTTCTTCTT 3353

Qy 1508 TTTTG 1512
 Db 3354 TTTTG 3358

RESULT 13
 ; Sequence 1, Application US/09061702
 ; Patent No. 6165737
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Xiaodong
 ; APPLICANT: Liu, Xuesong
 ; TITLE OF INVENTION: DNA FRAGMENTATION FACTOR INVOLVED IN

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OM nucleic - nucleic search, using sw model

Run on: July 10, 2004, 11:37:10 ; Search time 902 Seconds (without alignments)

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Title: US-09-813-492-1

Perfect score: 2017

Sequence: 1 tagataccctgaacctcc.....atacccaaaaaaaaaaa 2017

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Gapop 10.0 , Gapext 1.0

Searched: 3183909 seqs, 2436941669 residues

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Minimum DB seq length: 0

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Post-processing: Maximum Match 100% Listing First 45 summaries

Database : Published Applications NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2017	100.0	2017	9	US-09-813-492-1
2	1035.2	51.3	3117	9	US-09-834-795A-6
3	1035.2	51.3	3117	10	US-09-834-794A-6
4	542.2	26.9	643	15	US-10-106-698-1194
5	501.8	24.9	698	13	US-10-296-115-255
6	498	24.7	731	9	US-03-894-751A-5
7	498	24.7	731	15	US-10-146-496-1
8	497	24.6	768	9	US-09-931-381A-1
9	418.6	20.8	904	10	US-09-814-353-21771
10	369.6	18.3	496	15	US-10-166-496-3
C 11	361.8	17.9	472	9	US-09-964-824A-56
C 12	361.8	17.9	472	10	US-09-873-367C-175
C 13	356.4	17.9	533	15	US-10-023-386-4899
C 14	354.8	17.6	411	10	US-09-918-995-35876

%

Result No.	Score	Query Match	Length	DB ID	Description
1	2017	9	US-09-813-492-1	Sequence 1, Appli	Sequence 1, Appli
2	1035.2	51.3	3117	9	US-09-834-795A-6
3	1035.2	51.3	3117	10	US-09-834-794A-6
4	542.2	26.9	643	15	US-10-106-698-1194
5	501.8	24.9	698	13	US-10-296-115-255
6	498	24.7	731	9	US-03-894-751A-5
7	498	24.7	731	15	US-10-146-496-1
8	497	24.6	768	9	US-09-931-381A-1
9	418.6	20.8	904	10	US-09-814-353-21771
10	369.6	18.3	496	15	US-10-166-496-3
C 11	361.8	17.9	472	9	US-09-964-824A-56
C 12	361.8	17.9	472	10	US-09-873-367C-175
C 13	356.4	17.9	533	15	US-10-023-386-4899
C 14	354.8	17.6	411	10	US-09-918-995-35876

Result No.	Score	Query Match	Length	DB ID	Description
1	2017	9	US-09-813-492-1	Sequence 1, Appli	Sequence 1, Appli
2	1035.2	51.3	3117	9	US-09-834-795A-6
3	1035.2	51.3	3117	10	US-09-834-794A-6
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7	498	24.7	731	15	US-10-146-496-1
8	497	24.6	768	9	US-09-931-381A-1
9	418.6	20.8	904	10	US-09-814-353-21771
10	369.6	18.3	496	15	US-10-166-496-3
C 11	361.8	17.9	472	9	US-09-964-824A-56
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C 13	356.4	17.9	533	15	US-10-023-386-4899
C 14	354.8	17.6	411	10	US-09-918-995-35876

Result No.	Score	Query Match	Length	DB ID	Description
1	2017	9	US-09-813-492-1	Sequence 1, Appli	Sequence 1, Appli
2	1035.2	51.3	3117	9	US-09-834-795A-6
3	1035.2	51.3	3117	10	US-09-834-794A-6
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8	497	24.6	768	9	US-09-931-381A-1
9	418.6	20.8	904	10	US-09-814-353-21771
10	369.6	18.3	496	15	US-10-166-496-3
C 11	361.8	17.9	472	9	US-09-964-824A-56
C 12	361.8	17.9	472	10	US-09-873-367C-175
C 13	356.4	17.9	533	15	US-10-023-386-4899
C 14	354.8	17.6	411	10	US-09-918-995-35876

ALIGNMENTS

Result No.	Score	Query Match	Length	DB ID	Description
1	2017	9	US-09-813-492-1	Sequence 1, Appli	Sequence 1, Appli
2	1035.2	51.3	3117	9	US-09-834-795A-6
3	1035.2	51.3	3117	10	US-09-834-794A-6
4	542.2	26.9	643	15	US-10-106-698-1194
5	501.8	24.9	698	13	US-10-296-115-255
6	498	24.7	731	9	US-03-894-751A-5
7	498	24.7	731	15	US-10-146-496-1
8	497	24.6	768	9	US-09-931-381A-1
9	418.6	20.8	904	10	US-09-814-353-21771
10	369.6	18.3	496	15	US-10-166-496-3
C 11	361.8	17.9	472	9	US-09-964-824A-56
C 12	361.8	17.9	472	10	US-09-873-367C-175
C 13	356.4	17.9	533	15	US-10-023-386-4899
C 14	354.8	17.6	411	10	US-09-918-995-35876

Result No.	Score	Query Match	Length	DB ID	Description
1	2017	9	US-09-813-492-1	Sequence 1, Appli	Sequence 1, Appli
2	1035.2	51.3	3117	9	US-09-834-795A-6
3	1035.2	51.3	3117	10	US-09-834-794A-6
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7	498	24.7	731	15	US-10-146-496-1
8	497	24.6	768	9	US-09-931-381A-1
9	418.6	20.8	904	10	US-09-814-353-21771
10	369.6	18.3	496	15	US-10-166-496-3
C 11	361.8	17.9	472	9	US-09-964-824A-56
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C 13	356.4	17.9	533	15	US-10-023-386-4899
C 14	354.8	17.6	411	10	US-09-918-995-35876

Result No.	Score	Query Match	Length	DB ID	Description
1	2017	9	US-09-813-492-1	Sequence 1, Appli	Sequence 1, Appli
2	1035.2	51.3	3117	9	US-09-834-795A-6
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C 13	356.4	17.9	533	15	US-10-023-386-4899
C 14	354.8	17.6	411	10	US-09-918-995-35876

Result No.	Score	Query Match	Length	DB ID	Description
1	2017	9	US-09-813-492-1	Sequence 1, Appli	Sequence 1, Appli
2	1035.2	51.3	3117	9	US-09-834-795A-6
3	1035.2	51.3	3117	10	US-09-834-794A-6
4	542.2	26.9	643	15	US-10-106-698-1194
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7	498	24.7	731	15	US-10-146-496-1
8	497	24.6	768	9	US-09-931-381A-1
9	418.6	20.8	904	10	US-09-814-353-21771
10	369.6	18.3	496	15	US-10-166-496-3
C 11	361.8	17.9	472	9	US-09-964-824A-56
C 12	361.8	17.9	472	10	US-09-873-367C-175
C 13	356.4	17.9	533	15	US-10-023-386-4899
C 14	354.8	17.6	411	10	US-09-918-995-35876

Result No.	Score	Query Match	Length	DB ID	Description
1	2017	9	US-09-813-492-1	Sequence 1, Appli	Sequence 1, Appli
2	1035.2	51.3	3117	9</	

Db	181	TCATGCTCCAGGCTTCAAGAGCTTCCATATTGCTTCAGAAGCTTCAAGATGCTCCAGA 240	Db	1261	GTGATTCCTGCCTAGCCCTCAAGTAATGATAATTACGGCGCCAGCCACACCC 1320
Qy	241	GGAGGTTTCACATCATATTCCAGAGCTCTGGAAAGTGAATAATGTTGCTGATCCA 300	Qy	1321	CCGCTGATTTTGTTTATTTTATGAGACGACGGGTTTCCCAAGCTTGGCGGTGGCTTC 1380
Db	241	GGAGGTTTCACATCATATTCCAGAGCTCTGGAAAGTGAATAATGTTGCTGATCCA 300	Db	1321	CCGCTGATTTTGTTTATGAGACGACGGGTTTCCCAAGCTTGGCGGTGGCTTC 1380
Qy	301	GAGAGCTGATGGGATTGTTGACTTGGCTCATCTTCATGTCAGGCAGAGAAAT 360	Qy	1381	AAACTCTTGACCTCAAGTGAACCCCGCTGCTCCCAAAAGTCTGGATAATCAGC 1440
Db	301	GAGAGCTGATGGGATTGTTGACTTGGCTCATCTTCATGTCAGGCAGAGAAAT 360	Db	1381	AAACTCTTGACCTCAAGTGAACCCCGCTGCTCCCAAAAGTCTGGATAATCAGC 1440
Qy	361	CTGTGTAGCCGCAZACCATACTGTTAACGATGTCAGTGAAGTGGCCAGAA 420	Qy	1441	GTGAGCCACCATGCGGGCTCAACAGCTTGAATGTTGAGTGTATACTTGCCTTTG 1500
Db	361	CTGTGTAGCCGCAZACCATACTGTTAACGATGTCAGTGAAGTGGCCAGAA 420	Db	1441	GTGAGCCACCATGCGGGCTCAACAGCTTGAATGTTGAGTGTATACTTGCCTTTG 1500
Qy	421	AAATGGTAAGGAAATTGTCACAGGAAGAACACATGGCAAGGAAACAGTACAG 480	Qy	1501	GCCTCTTTTGTCCATAGGGCTTCAAGATAAGTATGGTAAGGGCAAGCTAGTGTTCATA 1560
Db	421	AAATGGTAAGGAAATTGTCACAGGAAGAACACATGGCAAGGAAACAGTACAG 480	Db	1501	GCCTCTTTTGTCCATAGGGCTTCAAGATAAGTATGGTAAGGGCAAGCTAGTGTTCATA 1560
Qy	481	GGCACATCAGGGAAAACAGAAACATAGGGCCATAAAACTCCATTAGAGTCTACAG 540	Qy	1561	AGAGGCCAATAGAGCAGGAGGGCCACATTATGGTGGCAAGTGTGCTCCCTGC 1620
Db	481	GGCACATCAGGGAAAACAGAAACATAGGGCCATAAAACTCCATTAGAGTCTACAG 540	Db	1561	AGAGGCCAATAGAGCAGGAGGGCCACATTATGGTGGCAAGTGTGCTCCCTGC 1620
Qy	541	ATAAATCTACAGAGACATTCTCAAGTGGACTTGGCATATTGTTGTAAGTTTATCA 600	Qy	1681	AGGCACATGAGTCCTCATAGTTAAATGGCCATAAAACTGGCTTTCCTCTTC 1740
Db	541	ATAAATCTACAGAGACATTCTCAAGTGGACTTGGCATATTGTTGTAAGTTTATCA 600	Db	1681	AGGCACATGAGTCCTCATAGTTAAATGGCCATAAAACTGGCTTTCCTCTTC 1740
Qy	601	TCTGAATTCTCTTATGTCACAGCAACAAATAATTGTTTAAATGTA 660	Qy	1801	TATTTCCACTTTAGATGAGAAATTGAGCTCTTAGCTTAAGCTAAATGCTTC 1740
Db	601	TCTGAATTCTCTTATGTCACAGCAACAAATAATTGTTTAAATGTA 660	Db	1801	TATTTCCACTTTAGATGAGAAATTGAGCTCTTAGCTTAAGCTAAATGCTTC 1740
Qy	661	ACAAATTGGCGSTPAGCAAGTAACTCAAACTCTGGCTTCAAGGGAT 720	Qy	1861	TCAACAGGAAGTGGAGAGACAAGCTTAAATAGAAATAATTAATAATAATAATA 1920
Db	661	ACAAATTGGCGSTPAGCAAGTAACTCAAACTCTGGCTTCAAGGGAT 720	Db	1861	TCAACAGGAAGTGGAGAGACAAGCTTAAATAGAAATAATTAATAATAATAATA 1920
Qy	721	CCTCCCCACCTTACGCTCCAAAGTACTGGGATTATAGCTGTCAGTGCCT 780	Qy	1921	TGAGATAACTAAATAATTAAATAACCAATAATTAAACCGTGTAAACCAA 1980
Db	721	CCTCCCCACCTTACGCTCCAAAGTACTGGGATTATAGCTGTCAGTGCCT 780	Db	1921	TGAGATAACTAAATAATTAAATAACCAATAATTAAACCGTGTAAACCAA 1980
Qy	781	AATTATTCCTGTGATAAACTCAGGTTAAATGTTGGTTAAGGATTTCCTACGTGA 840	Qy	1981	CATTAAATAAAACTTAAGCTTAAACCAAAACCAAAACCAAAACCAAAACCAAA 2017
Db	781	AATTATTCCTGTGATAAACTCAGGTTAAATGTTGGTTAAGGATTTCCTACGTGA 840	Db	1981	CATTAAATAAAACTTAAGCTTAAACCAAAACCAAAACCAAAACCAAAACCAAA 2017
Qy	841	ATTCTGTGACTATTCTCATTTAGCTTAAATTTAGGTATTCTAAATAG 900	Qy	901	AATAGTTAAACTAAATAACTCTAAACAGCTCTAGTTGAGTACCGTTGTTGGA 960
Db	841	ATTCTGTGACTATTCTCATTTAGCTTAAATTTAGGTATTCTAAATAG 900	Db	901	AATAGTTAAACTAAATAACTCTAAACAGCTCTAGTTGAGTACCGTTGTTGGA 960
Qy	961	TTGAAATTTCCTGATCATCTGAAAGAAAAAAGCCCTGCGCTTCCTG 1020	Qy	961	TTGAAATTTCCTGATCATCTGAAAGAAAAAAGCCCTGCGCTTCCTG 1020
Db	961	TTGAAATTTCCTGATCATCTGAAAGAAAAAAGCCCTGCGCTTCCTG 1020	Db	1021	CTCCCCCAGTCAGTCAGTTAGCTGCTAAACAGAGGCTTACATCTTGTGT 1080
Qy	1021	CTCCCCCAGTCAGTCAGTTAGCTGCTAAACAGAGGCTTACATCTTGTGT 1080	Qy	1081	GGTGGATTTCACGCTCTGGCTAAACAGAGGCTTACATCTTGTGT 1140
Db	1021	CTCCCCCAGTCAGTCAGTTAGCTGCTAAACAGAGGCTTACATCTTGTGT 1080	Db	1081	GGTGGATTTCACGCTCTGGCTAAACAGAGGCTTACATCTTGTGT 1140
Qy	1141	CTCACACGGCTGGAGTCAGTCAGTCAGTTAGCTGCTTCTGGCTTCCTG 1200	Qy	1141	CTCACACGGCTGGAGTCAGTCAGTCAGTTAGCTGCTTCTGGCTTCCTG 1200
Db	1141	CTCACACGGCTGGAGTCAGTCAGTTAGCTGCTTCTGGCTTCCTG 1200	Db	1201	CCAGGGCTGGAGTCAGTCAGTCAGTCAGTTAGCTGCTTCTGGCTTCCTG 1260
Qy	1201	CCAGGGCTGGAGTCAGTCAGTCAGTCAGTCAGTTAGCTGCTTCTGGCTTCCTG 1260	Qy	1201	CCAGGGCTGGAGTCAGTCAGTCAGTCAGTCAGTTAGCTGCTTCTGGCTTCCTG 1260
Db	1201	CCAGGGCTGGAGTCAGTCAGTCAGTCAGTCAGTTAGCTGCTTCTGGCTTCCTG 1260	Db	1261	GTGATTCCTGGCTCAAGCTGCTTCAAGTAATGATAATTACGGCCAGCACCAACC 1320
Qy	1261	GTGATTCCTGGCTCAAGCTGCTTCAAGTAATGATAATTACGGCCAGCACCAACC 1320	Qy	1261	GTGATTCCTGGCTCAAGCTGCTTCAAGTAATGATAATTACGGCCAGCACCAACC 1320

RESULT 2
US-09-134-795A-6
; Sequence 6, Application US/09834795A
; Patent No. US20020020076710A1
; GENERAL INFORMATION:
; APPLICANT: Lyn, Dyster
; APPLICANT: Jana, Frusaci
; TITLE OF INVENTION: Detection and Treatment of Breast Cancer
; FILE REFERENCE: 3380/11127-US3
; CURRENT APPLICATION NUMBER: US/09/834,795A
; CURRENT FILING DATE: 2001-04-12
; PRIORITY APPLICATION NUMBER: 09/146,580
; PRIORITY FILING DATE: 1998-09-03
; PRIORITY APPLICATION NUMBER: 60/071,899
; PRIORITY FILING DATE: 1998-01-20
; PRIORITY APPLICATION NUMBER: 60/092,155
; PRIORITY FILING DATE: 1998-07-09
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 3117

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
 LOCATION: (1) .. (3117)
 OTHER INFORMATION: n at any position in the sequence represents a or g or c or t/u
 NAME/KEY: unsure
 LOCATION: (1) .. (3117)
 OTHER INFORMATION: y at any position in the sequence represents t/u or c
 NAME/KEY: unsure
 LOCATION: (1) .. (3117)
 OTHER INFORMATION: m at any position in the sequence represents a or c
 NAME/KEY: unsure
 LOCATION: (1) .. (3117)
 OTHER INFORMATION: k at any position in the sequence represents g or t/u
 NAME/KEY: unsure
 LOCATION: (1) .. (3117)
 OTHER INFORMATION: s at any position in the sequence represents g or c
 NAME/KEY: unsure
 LOCATION: (1) .. (3117)
 OTHER INFORMATION: w at any position in the sequence represents a or t/u
 NAME/KEY: unsure
 LOCATION: (1) .. (3117)
 OTHER INFORMATION: r at any position in the sequence represents g or a
 US-09-834-195A-6

Query Match 51.3% ; Score 1035.2 ; DB 9 ; Length 3117;
Best Local Similarity 86.5% ; Pred. No. 1..3e-231 ;
Matches 1172 ; Conservative 73 ; Mismatches 92 ; Indels 18 ; Gaps 15 ;

Qy 671	GGTATGAAATGTAGCCATAATAATCTCAAATCCGGCAAGGATCCCTCCACCT	730	Db 1669	GCTCTCACTATGTTGCCCGGTGATCTCAACTCCGGCTCAGGGTCTCCACCT	1728
Qy 731	TAGCCTCCAACTACTGGGATAATAGGTGAGGCCAACAGTGGCTGCCTAAATTTC	790	Db 1729	TAGCCTCCAAAGTACTGGGATAATAGGTGAGGCCAACAGTGGCTGCCTAAATTTC	1788
Qy 791	TGTGATGAAATCAGGTTTAATGTTCTAGATTTCTACGTGATTCGTCAC	950	Db 1789	TGTGATGAAATCAGGTTTAATGTTCTACGTGATTCGTCAC	1848
Qy 851	TATTTGCAATTAGAGTTCAAAATATAGGGTTATTTCTAAATAAGAATGTTA	910	Db 1849	TATTTGCAATTAGAGTTCAAAATATAGGGTTATTTCTAAATAAGAATGTTA	1908
Qy 911	ACTAAATAACTCTAAAGCTCTAGTTGAGTGTACGGTTGGATGAAATT	970	Db 1909	ACTAAATAACTCTAAAGCTCTAGTTGAGTGTACGGTTGGATGAAATT	1968
Qy 971	CTGATACGAAAGAACAAAACCTTTTGCCTCCCCAGT	1030	Db 1969	CTGATACGAAAGAACAAAACCTTTTGCCTCCCCAGT	2028
Qy 1031	CAGTCTGAGGAGGACTAGTGTAGGGCCCAAGTGTGGCTCTGTTGTTGATTTA	1090	Db 2029	NAATTCCTGNGCAAGTAACTGGGNCWACATTTAGCTCCTATTCCACCTT	2088
Qy 1091	TGTGTTGTTGGTTGGTTGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1150	Db 2089	NGTCTGCTAAACAGGGCNWACATTTAGCTCCTATTCCACCTT	2148
Qy 1151	TTGTTGTTGGTTGGTTGGTTGGTGTGTTGTTGTTGTTGTTGTTGTTGTTG	1209	Db 2149	TTTCTGTTGGTGTGTTGGTTGGTGTGTTGTTGTTGTTGTTGTTGTTG	2207
Qy 1210	AG-TGGAGGGCACATCTGGT-CATGCCAACCTCCCTCCCGT-UGTGTAGCTG	1265	Db 2208	ARTGCAAGTGGCACATCTGGT-CATGCCAACCTCCCTCCCGT-UGTGTAGCTG	2267
Qy 1266	TCTCTGCTCAGCT-CCCAAGTACTGATATTACGCCAGCCAGCACCACCCCG	1324	Db 2268	YTCCTGCTCAGCTCAGTCCAAAGTAATTACAGGNGCCACCCAGCACCACCCGN	2327

RESULT 3
US-09-834-195A-6
; sequence 6 , Application US/09834794A
; Publication No. US200300267771
; GENERAL INFORMATION:
 ; APPLICANT: Jana, Frustaci
 ; INVENTION: Detection and Treatment of Breast Cancer
 ; FILE REFERENCE: 3380/11127-054
 ; CURRENT APPLICATION NUMBER: US/09/834,794A
 ; CURRENT FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 09/146,580
 ; PRIOR FILING DATE: 1998-09-03
 ; PRIOR APPLICATION NUMBER: 60/071,899
 ; PRIOR FILING DATE: 1998-01-20
 ; PRIOR APPLICATION NUMBER: 60/092,155
 ; PRIOR FILING DATE: 1998-07-09
 ; NUMBER OF SEQ ID NOS: 35
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 6
 ; LENGTH: 3117
 ; TYPE: DNA

NAME/KEY: mat_peptide
 LOCATION: (122)...()

OTHER INFORMATION:
 NAME/KEY: misc_feature
 LOCATION: (529)...(529)

OTHER INFORMATION: unknown amino; may be "A", "C", or "G"
 US-09-898-751A-5

Query Match 24.7%: Score 498; DB 9; Length 731;
 Best Local Similarity 100.0%; Pred. No. 3.5e-106;
 Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 CTGATCGAACAGCCCTCACTGTGTCGTGCACTGCCAGTAGGGCAGGAATGCCAGC 152
 Db 3 CTGATCGAACAGCCCTCACTGTGTCGTGCACTGCCAGTAGGGCAGGAATGCCAGC 62

QY 153 AGAGAGGACTGCCATGTGCCCTGGCTGCTGGGCCCTCATGCCCTCAGGCCA 212
 Db 63 AGAGAGGACTGCCATGTGCCCTGGCTGCTGGGCCCTCATGCCCTCAGGCCA 122

QY 213 TACTTCCATTCGCTTCAGCTGTGCAAGGGATTTACATCATATTCCAGAACGCC 272
 Db 123 TACTTCCATTCGCTTCAGCTGTGCAAGGGATTTACATCATATTCCAGAACGCC 182

QY 273 TGGAAAGAGTGTGAAATATGTGTGCACTGCCAGAGCTGTGACTTGGCTGCTG 332
 Db 183 TGGAAAGAGTGTGAAATATGTGTGCACTGCCAGAGCTGTGACTTGGCTGCTG 242

QY 333 TCATCCTCATGTGCAAGCCGAGAAATCTGTAGCCGCACACATACGTGTAAGC 392
 Db 243 TCATCCTCATGTGCAAGCCGAGAAATCTGTGCAACACATACGTGTAAGC 302

QY 393 AGTGGATGAAAGTGTGCAAGCTTCAGAGCTGTGACTTGGCTGACAGGAGA 452
 Db 303 AGTGGATGAAAGTGTGCAAGCTTCAGAGCTGTGACTTGGCTGACAGGAGA 362

QY 453 AACACCATGCCAAGGAAACAGTAACTAGGGCACATCAGGGAAACAGAAACATAGGCC 512
 Db 363 AACACCATGCCAAGGAAACAGTAACTAGGGCACATCAGGGAAACAGAAACATAGGCC 422

QY 513 ATAAAACCTCCATTAGAGAGTCTACAGATAAATCTACAGAGCATTCAGTGAC 572
 Db 423 ATAAAACCTCCATTAGAGAGTCTACAGATAAATCTACAGAGCATTCAGTGAC 482

QY 573 TTGGCCATGATTGGTT 590
 Db 483 TTGGCCATGATTGGTT 500

RESULT 7 US-10-146-496-1
 TITLE OF INVENTION: Mammalian Chemokines
 NUMBER OF SEQUENCES: 12
 Publication No. US20030031646A1
 GENERAL INFORMATION:
 ADDRESSEE: DNAX Research Institute
 STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:

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QY 513 ATAAACTCTTATAGAGGTCTACAGATAAATTACAGAGACATTCTCAAGTGGAC 573
Db 423 ATAAACTCTTATAGAGGTCTACAGATAAATTACAGAGACATTCTCAAGTGGAC 482

QY 573 TTGGCCATGATGGTTGT 590
Db 483 TTGGCCATGATGGTTGT 500

RESULT 8
US-09-331-381A-1
; Sequence 1, Application US/09931381A
; Patent No. US20020137107A1
; GENERAL INFORMATION:
; APPLICANT: Butcher, Eugene C.
; APPLICANT: Kunkel, Eric J.
; APPLICANT: Pan, Junliang
; APPLICANT: Soler-Ferran, Dulce
; TITLE OF INVENTION: Method for Identifying Agents Which
; Modulate Chemokine "MEC"-Induced Functions of CCR3 and/
; TITLE OF INVENTION: CCR10
; FILE REFERENCE: 1855-2010-003
; CURRENT APPLICATION NUMBER: US 09/931,381A
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: U.S. 09/638,914
; PRIOR FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (53) . . . (436)
US-09-331-381A-1

Query Match 24.6%; Score 497; DB 9; Length 768;
Best Local Similarity 100.0%; Pred. No. 6.2e+06;
Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 94 TGTATGCCAGCCCTACCTGGTCTGTCAGTGGCACTAGGCAGGAAATGCA 153
Db 1 TGTATGCCAGCCCTACCTGGTCTGTCAGTGGCACTAGGCAGGAAATGCA 60
Qy 154 GAGGAGACTGCCATGTGCCCTGGCTCTGGGCCCTCATGGCTCAGAAGGCCAT 213
Db 61 GAGGAGACTGCCATGTGCCCTGGCTCTGGGCCCTCATGGCTCAGAAGGCCAT 120
Qy 214 ACTTCCTATGGCTCAGCTGGTCAAGGGTTTCACTCATATTCAGAGGTCTCT 273
Db 121 ACTTCCTATGGCTCAGCTGGTCAAGGGTTTCACTCATATTCAGAGGTCTCT 180
Qy 274 GGAAGGTGAATATGGTGTGATTCAGAGGTGATGGGATTGACTTGGCTGT 333
Db 181 GGAAGGTGAATATGGTGTGATTCAGAGGTGATGGGATTGACTTGGCTGT 240
Qy 334 CATCCCTCATGGCAAGCCAGAGAATCTGGTCTGAGCCGACAAACCATACGGTTAACGA 393
Db 241 CATCCCTCATGGCAAGCCAGAGAATCTGGTCTGAGCCGACAAACCATACGGTTAACGA 300
Qy 394 GTGGATGAAAGTGGCAAGTGGCCAGAAGTGGTAAGGAATGTGTGCCAAGGAGGAA 453
Db 301 GTGGATGAAAGTGGCAAGTGGCCAGAAGTGGTAAGGAATGTGTGCCAAGGAGGAA 360
Qy 454 ACACCATGGCAAGGACAGTAACGGCACATCGGGAAACACGGAAACATACGGCCA 513
Db 361 ACACCATGGCAAGGACAGTAACGGCACATCGGGAAACACGGAAACATACGGCCA 420
Qy 514 TAAACACTCTTATTAGAGGCTTACAGATAAATCTACAGAGACAAATTCCTCAAGTGA 573
Db 421 TAAACACTCTTATTAGAGGCTTACAGATAAATCTACAGAGACAAATTCCTCAAGTGA 480

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QY 574 TGGCCATGATTGGTGT 590
 US-09-814-353-21771
 Sequence 21771, Application US/09814353
 Publication No. US20030165831A1
 GENERAL INFORMATION:
 APPLICANT: Lee, John
 APPLICANT: Thompson, Pamela
 APPLICANT: Lillie, James
 TITLE OF INVENTION: NOVEL GENES, COMPOSITES
 TITLE OF INVENTION: IDENTIFICATION AS
 TITLE OF INVENTION: IDENTIFICATION OF OVARIAN
 FILE REFERENCE: MRI - 006B
 CURRENT APPLICATION NUMBER: US/09/814,3
 CURRENT FILING DATE: 2001-03-21
 PRIORITY NUMBER: US 60/191,031
 PRIORITY NUMBER: US 60/191,031
 PRIORITY NUMBER: US 60/207,124
 PRIORITY NUMBER: US 60/207,124
 PRIORITY NUMBER: US 60/211,945
 PRIORITY NUMBER: US 60/211,945
 PRIORITY NUMBER: US 60/216,820
 PRIORITY NUMBER: US 60/216,820
 PRIORITY NUMBER: US 60/220,661
 PRIORITY NUMBER: US 60/220,661
 PRIORITY NUMBER: US 60/257,672
 PRIORITY NUMBER: US 60/257,672
 NUMBER OF SEQ ID NOS: 22037
 SOFTWARE: Fast-SEQ for Windows Version 4
 SEQ ID NO: 21771
 LENGTH: 904
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1, 2, 3, 4, 5, 6, 7, 8, 9, 9
 OTHER INFORMATION: n = A, T, C or G
 US-09-814-353-21771

Query Match 20.8% Score 41
 Best Local Similarity 95.8% Pred. No
 Matches 474; Conservative 0; Misma

QY 201 CCTCAAGGCTCTGGAAAGAGTGAATAT
 Db 97 CCTCAACCAACCATCTTCCATGCTTC
 QY 261 CCAGAAAGGCTCTGGAAAGAGTGAATAT
 Db 157 CCAGAAAGGCTCTGGAAAGAGTGAATAT
 QY 321 ACTGGGTGCTGTCACTCCTCATGCTCA
 Db 217 ACTGGGTGCTGTCACTCCTCATGCTCA
 QY 381 ATACTGTTAAGGTAAGGTGTGAAAGTGC
 Db 277 ATACTGTTAAGGTAAGGTGTGAAAGTGC
 QY 441 GGCACAGGAAAGAAACCATGCCAAGAG
 Db 337 GGCACAGGAAAGAAACCATGCCAAGAG
 QY 501 AAACATAGGCCATAAAACTCCTTATA
 Db 397 AAACATAGGCCATAAAACTCCTTATA
 QY 561 CCTCAAGGCTCTGGAAAGAGTGAATAT -- GG

Db 457 CCTCAAGTGGACTTGGCATGATTGGTAAAGTTTATCCTGAAATTCTCCCTTA-TG 515
 QY 619 TGGACACAGACACAAACAAATAATTGTTTTTAAAGAA---TGAACAAATTGTT-CGCTA 674
 Db 516 GAGACACAGACAAACAAATAATTGTTTTAAACAACTGAACCAATTGTGCCGTTA 575
 QY 675 TGGAAATTGAGCCAA 689
 Db 576 TGGAAATTGAGCCAA 590

RESULT 10
 US-10-146-496-3
 i Sequence 3, Application US/10146496
 i Publication No. US20030031446A1
 i GENERAL INFORMATION:
 i i APPLICANT: Vicari, Alain
 i i i Morales, Janine M.
 i i i Hurdick, Joseph A.
 i i i Zioltok, Albert
 i i i TITLE OF INVENTION: Mammalian Chemokines
 i i i NUMBER OF SEQUENCES: 12
 i i i CORRESPONDENCE ADDRESS:
 i i i ADDRESSEE: DNAX Research Institute
 i i i STREET: 901 California Avenue
 i i i CITY: Palo Alto
 i i i COUNTRY: USA
 i i i ZIP: 94304-1104
 i COMPUTER READABLE FORM:
 i i MEDIUM TYPE: Floppy disk
 i COMPUTER: IBM PC compatible
 i OPERATING SYSTEM: PC-DOS/MS-DOS
 i SOFTWARE: Patentin Release #1.0, Version #1.30
 i CURRENT APPLICATION DATA:
 i i APPLICATION NUMBER: US/10/146,496
 i i FILING DATE: 15-MAY-2002
 i i CLASSIFICATION: <Unknown>
 i i PRIORITY APPLICATION DATA:
 i i i APPLICATION NUMBER: US/08/978,964A
 i i i FILING DATE: 26-NOV-1997
 i i i APPLICATION NUMBER: US xx/xxx,xxx
 i i i FILING DATE: 24-OCT-1997
 i i ATTORNEY/AGENT INFORMATION:
 i i i NAME: Ching, Edwin P.
 i i i REGISTRATION NUMBER: 34,090
 i i i REFERENCE/DOCKET NUMBER: DX0684K1
 i i TELEPHONE: (650)852-5196
 i i INFORMATION FOR SEQ ID NO: 3:
 i i i SEQUENCE CHARACTERISTICS:
 i i i LENGTH: 496 base pairs
 i i i TYPE: nucleic acid
 i i i STRANDEDNESS: single
 i i i TOPOLOGY: linear
 i i i MOLECULE TYPE: cDNA
 i i i SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 i i i i US-10-146-496-3

Query Match 18.3%; Score 369.6; DB 15; Length 496;
 Best Local Similarity 85.0%; Pred. No. 3.3e-76; Indels 4; Gaps 2;
 Matches 420; Conservative 0; Mismatches 70;

QY 91 TCTGTATGAAACGCCCACTTGCTGCTGCAAGTCCAGTGGGGAGGAGATGCA 150
 1 TCTGTATGAAACGCCCACTTGCTGCTGCAAGTCCAGTGGGGAGGAGATGCA 60

QY 151 GGGAGGGACTGGCCATGGCTGCTGCGGCGCTACATGGCTCAAGC 210
 61 GGAGAGGGACTGGCCATGGCTGCTGCGGCGCTACATGGCTCAAAAGC 120

Db 121 CATACTCCATTGCCAGCTGTCAGGAGGTCACTATTCCAGAAGGCT 180
 QY 271 CCT-GGAAAGTGTAAATGTTGTCATCCAGAGCTGATGGGATTTGACTGGCTG 329
 Db 181 CCTGGCAAAGATGAAATATGTGTCATCCAGAGCTGATGGGATTTGACTGGCTG 240
 QY 330 CTGTGATCCCTCATGTCAGGAAATCTGTCTAGCCGACAACTACTGTTA 389
 Db 241 CTGTGATCCCTCATGTCAGGAAAGATCTGTCTAGCCGACAACTACTGTTA 300
 QY 390 AGCAGTGGTAAAGTGCAGCTGCCAAGAAATAATGTTAAGGAATGTTGCAAGGA 449
 Db 301 AGCAGTGGNTAAAGTGCAGGAAATAATGTTAAGGAATTTCCACAGGG 360
 QY 450 AG--AAACACCATGGCAAGGAACTGAAAGTCAAGGGCACATCAAGGGAAACAT 506
 Db 361 NGGAAACACCCGTGGNAAGGGGAACTGGGACTTGGGAAANGGGAAANT 420
 QY 507 ACGGCATAAAACTCCTTATTAGAGTCTACAGATAATCTACAGAGAAATCTCTCAA 566
 Db 421 NGGCTNTAAATACTCCTTATTNGGGNTTTAAGGTTAAATTNNNGGAAATTTCCTNA 480
 QY 567 GTGGACTTGGCCAT 580
 Db 481 GGGNTTTGGNCAT 494

RESULT 11
 US-09-964-824A-56/c
 i Sequence 56, Application US/09964824A
 i i Patent No. US2002012531A1
 i GENERAL INFORMATION:
 i i APPLICANT: Horrigan, Stephen
 i i i TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signat
 i i i i CURRENT APPLICATION NUMBER: US/09/964, 824A
 i i i i CURRENT FILING DATE: 2001-09-27
 i i i i PRIORITY APPLICATION NUMBER: US/60/236,033
 i i i i PRIORITY FILING DATE: 2000-09-28
 i i i i PRIORITY APPLICATION NUMBER: US/60/236,032
 i i i i PRIORITY FILING DATE: 2000-09-28
 i i i i PRIORITY APPLICATION NUMBER: US/60/236,028
 i i i i PRIORITY FILING DATE: 2000-09-28
 i i i i NUMBER OF SEQ ID NOS: 583
 i i i i SEQ ID NO: 56
 i i i i TYPE: DNA
 i i i i ORGANISM: Homo sapiens
 i i i i FEATURE:
 i i i i NAME/KEY: misc_feature
 i i i i LOCATION: (1)...(472)
 i i i i OTHER INFORMATION: n,a,t,g or c
 i i i i US-09-964-824A-56

Query Match 17.9%; Score 361.6; DB 9; Length 472;
 Best Local Similarity 9.9-2%; Pred. No. 2.2e-74;
 Matches 374; Conservative 0; Mismatches 72; Indels 1; Gaps 1;
 QY 1633 AGGGGGGGTGTGTCAGGATGCTGGGGTGTATGGGACACAGAGGACATGAGTC 1692
 Db 471 AGGGTGTGTGTCAGGATGCTGGGGTGTATGGGACACAGAGCAGTC 412
 QY 1693 TCCATAGTTAAATG CCACCAAATCTGGCTTTCCTTATGACTATT 1751
 Db 411 TCCATAGTTAAATGCCCACAAACTGGCTTTCCTTATGACTATT 352
 QY 1752 AGGATTAATTATTTATTTCTGAACTTCTGAACTTCTGAACTTCTGAACTT 1811
 Db 351 GGAGTTAAATTATTTATTTCTGAACTTCTGAACTTCTGAACTTCTGAACTT 292

RESULT 14

US-09-918-95-35876

Sequence 35876, Application US/09918995

GENERAL INFORMATION:

APPLICANT: HYSEQ, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED FROM VARIOUS cDNA LIBRARIES

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 38976

LENGTH: 411

TYPE: DNA

ORGANISM: Homo sapiens

US-09-918-95-35876

Query Match 17 6%; Score 354.8; DB 10; Length 411;

Best Local Similarity 99.4%; Pred. No. 8.7e-73; Indels 0; Gaps 0;

Matches 356; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

Qy 201 CCTCAGAGCCCTACTTCCCATGGCTCCAGCTGTCACGGAGTTTCACATCATTT 260

Db 54 OCTCAACAGCCATACATTCCTCCATGGCTCCAGCTGTCACGGAGTTTCACATCATTT 113

Qy 261 CCAGAACGCTCTGGAAAGAGTGAATATGTGTGCATCCAGAGCTGATGGGATTGT 320

Db 114 CCAGAACGCTCTGGAAAGAGTGAATATGTGTGCATCCAGAGCTGATGGGATTGT 173

Qy 321 ACTTGCTGCTGCTCATCTTCATGTCAGGGAGAACATCTGTGTAAGCCGCACACC 380

Db 174 ACTTGCTGCTGCTCATCTTCATGTCAGGGAGAACATCTGTGTAAGCCGCACACC 233

Qy 381 ATACTGTTAACGGAGTGGATGAAAGTGGAGTGGCTAACAGAAAGAAAATGCTTAAGGAAATGTT 440

Db 234 ATACTGTTAACGGAGTGGATGAAAGTGGAGTGGCTAACAGAAAGAAAATGCTTAAGGAAATGTT 293

Qy 441 GGCACAGGAAGAAACCATGGGAAGGAAAGTGTACAGGACATCAGGGAAACACG 500

Db 294 GGCACAGGAAGAAACCATGGGAAGGAAACCATGGCAAGGGACATCAGGGAAACACG 353

Qy 501 AAACATACGGCCATAAAACTCCATTAGTAGAGTCTACAGATAAATTACAGAGACA 558

Db 354 AAACATACGGCCATAAAACTCCATTAGAGTCTACAGATAAATTACAGAGACA 411

Query Match 15 0%; Score 302; DB 9; Length 311;

Best Local Similarity 99.3%; Pred. No. 1.7e-60; Mismatches 0; Indels 0; Gaps 0;

Matches 302; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

Qy 208 AGCCATACCTCCATGGCTCCAGCTGTCACGGAGTTTCACATCATTTCCAGAAG 267

Db 311 AGCCATACCTCCATGGCTCCAGCTGTCACGGAGTTTCACATCATTTCCAGAAG 252

Qy 268 GCTCCCTGGAAAGAGTGAATATGTGTGCATCCAGAGCTGATGGGATGATGGATTGGC 327

Db 251 GCTCCCTGGAAAGAGTGAATATGTGTGCATCCAGAGCTGATGGGATGATGGATTGGC 192

Query Match 15 0%; Score 302; DB 9; Length 311;

Best Local Similarity 99.3%; Pred. No. 1.7e-60; Mismatches 0; Indels 0; Gaps 0;

Matches 302; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

Qy 328 TGCTGTCATCTTCATGTCAGGGAGAACATCTGTGCAAGGAAATGCTGTCACAG 387

Db 191 TGCTGTCATCTTCATGTCAGGGAGAACATCTGTGCAAGGAAATGCTGTCACAG 132

Qy 388 TAAGCAGTGGATGAAAGTGCAGGAAAGTGCAGGAAAGAAATGCTGTCACAG 447

Db 131 TAAGCAGTGGATGAAAGTGCAGGAAAGTGCAGGAAAGAAATGCTGTCACAG 72

Qy 448 GAAGAAACCATGGAAAGGAAAGCTAACGGACATCGGGAAACAGAAACATA 507

Db 71 GAAGAAACCATGGAAAGGAAAGCTAACGGACATCGGGAAACAGAAACATA 12

Search completed: July 10, 2004, 16:19:37

Job time : 905 secs

RESULT 15

US-09-834-795A-11/C

Sequence 11, Application US/09834795A

GENERAL INFORMATION:

APPLICANT: Lawrence, Papsidero

APPLICANT: Lynn, Pyster

APPLICANT: Jana, Frustaci

TITLE OF INVENTION: Detection and Treatment of Breast Cancer

FILE REFERENCE: 3380/11127-053

CURRENT APPLICATION NUMBER: US/09/834-795A

PRIOR APPLICATION NUMBER: 09/146,580

PRIOR FILING DATE: 1998-09-03

PRIOR APPLICATION NUMBER: 60/071,899

PRIOR FILING DATE: 1998-01-20

PRIOR APPLICATION NUMBER: 60/092,155

PRIOR FILING DATE: 1998-07-09